

---

**SEQUENCE LISTING:****(1) GENERAL INFORMATION:**

(i) APPLICANT: DUARTE CANO, C. A.  
GUILLÉN NIETO, G. E.  
MARTIN DUNN, A. M.  
ALVAREZ ACOSTA, A.  
CARPIO MUÑOZ, E. L.  
QUINTANA V. D.  
GOMEZ RODRIGUEZ, C. E.  
SILVA RODRIGUEZ, R. C.  
NAZBAL GILVEZ, C.  
LEAL ANGULO, M. J.

(ii) TITLE OF INVENTION: System for the expression of heterologous antigens as fusion proteins.

(iii) NUMBER OF SEQUENCES: 21

**(iv) CORRESPONDENCE ADDRESS:**

(A) ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan  
(B) STREET: One Chase Road  
(C) CITY: Scarsdale  
(D) STATE: New York  
(E) COUNTRY: U.S.  
(F) ZIP: 10583

**(v) COMPUTER READABLE FORM:**

(A) MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).  
(B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).  
(C) OPERATING SYSTEM: Windows 95.  
(D) SOFTWARE: Word Perfect 5.0 for Windows 95.

**(vi) CURRENT APPLICATION DATA:**

(A) APPLICATION NUMBER: 08/930,917  
(B) FILING DATE: 16-Sep-1997  
(C) CLASSIFICATION:

**(vii) PRIOR APPLICATION DATA:**

(A) APPLICATION NUMBER: PCT/CU97/00001  
(B) FILING DATE: 17-Jan-1997

**(viii) ATTORNEY/AGENT INFORMATION:**

(A) NAME: HENRY A. MARZULLO, JR.  
(B) REGISTRATION NUMBER: 20,910

(C) DOCKET NUMBER: P-13

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (914) 723-4300

(B) TELEFAX: (914) 723-4301

(C) E-MAIL: HMARZULLO@LSMAG.COM

(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
1                  5                  10                  15  
Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
                  20                  25                  30  
Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp  
                  35                  40                  45

(2) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:  
(A) NAME/KEY: 1573  
(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
TTCCATGGTA GATAAAAGAA TGGCTTTAG

29

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

**(vi) ORIGINAL SOURCE:****(A) ORGANISM:** *Neisseria meningitidis***(B) STRAIN:** B:4:P1.15**(vii) IMMEDIATE SOURCE:****(A) LIBRARY:** Genomic**(B) CLONE:** P64K**(ix) FEATURE:****(A) NAME/KEY:** 1575**(D) OTHER INFORMATION:** Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO: 3:

TTTCTAGATC CAAAGTAATC AGGGTATCG

29

**(2) INFORMATION FOR SEQ. ID NO: 4****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 26 base pairs**(B) TYPE:** Nucleic acid**(C) STRANDEDNESS:** Unknown**(D) TOPOLOGY:** Unknown**(ii) MOLECULE TYPE:** Other nucleic acid**(A) DESCRIPTION:** Synthetic oligonucleotide**(iii) HYPOTHETICAL:** No**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** -C Terminal fragment**(vi) ORIGINAL SOURCE:****(A) ORGANISM:** *Neisseria meningitidis***(B) STRAIN:** B:4:P1.15**(vii) IMMEDIATE SOURCE:****(A) LIBRARY:** Genomic**(B) CLONE:** P64K**(ix) FEATURE:****(A) NAME/KEY:** Primer 2192**(D) OTHER INFORMATION:** Primer 3' for PCR amplification of the first 120 amino acids of the

recombinant protein of *Neisseria meningitidis* P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
GGCGGTTCTG CCGATTAAGG ATCCGA

26

C

**(2) INFORMATION FOR SEQ. ID NO: 5****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 146 base pairs
- (B) TYPE:** Nucleic acid
- (C) STRANDEDNESS:** Unknown
- (D) TOPOLOGY:** Unknown

**(ii) MOLECULE TYPE:** Other nucleic acid**(A) DESCRIPTION:** Fragment amplified by PCR**(iii) HYPOTHETICAL:** Yes**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** -N-terminal fragment**(vi) ORIGINAL SOURCE:**

- (A) ORGANISM:** *Neisseria meningitidis*
- (B) STRAIN:** B:4:P1.15

**(vii) IMMEDIATE SOURCE:**

- (A) LIBRARY:** Genomic
- (B) CLONE:** P64K

**(ix) FEATURE:**

**(D) OTHER INFORMATION:** Fragment derived from the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K, containing a *Nco*I site at the position 3 to 8 and a *Xba*I site at the position 139 to 144

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:**

TTCCATGGTA GATAAAAGAA TGGCTTTAGT TGAATTGAAA GTGCCCGACA  
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AAACGTGGGC GACACTATTG  
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA  
146

**(2) INFORMATION FOR SEQ. ID NO: 6:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 47 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Stabilizer derived from the first 47 amino acids of the recombinant

protein of *Neisseria meningitidis* P64K, containing the following changes: L2 V2; E45 D45;

T46 L46; D47 E47.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :  
CTAGATTGGA TATCAG

16

(2) INFORMATION FOR SEQ. ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

GATCCTGATA TCAAAT

16

(2) INFORMATION FOR SEQ. ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: LR150

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation LR150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 10:

(A) SEQUENCE CHARACTERISTICS:

(B) LENGTH: 15 Amino acid residues

(C) TYPE: Amino acid

(D) STRANDEDNESS: Unknown

(E) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: JY1

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation JY1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: RF

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.

(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: MN

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation MN.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr  
1                    5                    10                    15

(2) INFORMATION FOR SEQ. ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: BRVA

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the

VIH-1, isolation BRVA.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Arg Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1


(C) INDIVIDUAL ISOLATE: IIIB

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation IIIB.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
1 5 10 15

**(2) INFORMATION FOR SEQ. ID NO: 15:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 15 Amino acid residues.**(B) TYPE:** Amino acid.**(C) STRANDEDNESS:** Unknown.**(D) TOPOLOGY:** Unknown.**(ii) MOLECULE TYPE:** Peptide**(iii) HYPOTHETICAL:** Yes**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** Internal fragment**(vi) ORIGINAL SOURCE:****(A) ORGANISM:** VIH-1**(ix) FEATURE:****(D) OTHER INFORMATION:** Consensus sequence of the central region of the loop V3 belongingto the protein gp120 obtained from different isolations of the VIH-1, position 7 within the  
multi-epitopic polypeptide (MEP) TAB13.**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:** Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly  
1                      5                      10                      15**(2) INFORMATION FOR SEQ. ID NO: 16:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 15 Amino acid residues**(B) TYPE:** Amino acid**(C) STRANDEDNESS:** Unknown**(D) TOPOLOGY:** Unknown**(ii) MOLECULE TYPE:** Peptide**(iii) HYPOTHETICAL:** Yes**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** Internal fragment**(vi) ORIGINAL SOURCE:**

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 8 within the multiepitopic polypeptide (MEP) TAB13.

C

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:**

Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Arg Leu Tyr Thr Thr  
1                      5                      10                      15

**(2) INFORMATION FOR SEQ. ID NO: 17:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 5 Amino acid residues**(B) TYPE:** Amino acid**(C) STRANDEDNESS:** Unknown**(D) TOPOLOGY:** Unknown**(ii) MOLECULE TYPE:** Peptide**(iii) HYPOTHETICAL:** No**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** Internal fragment**(ix) FEATURE:****(D) OTHER INFORMATION:** Flexible spacer separating epitopes V3 in the MEP

TAB3, TAB4,

TAB9 and TAB13.

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:**

Ala Gly Gly Gly Ala  
1                      5

**(2) INFORMATION FOR SEQ. ID NO: 18:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 141 Amino acid residues**(B) TYPE:** Amino acid**(C) STRANDEDNESS:** Unknown**(D) TOPOLOGY:** Unknown**(ii) MOLECULE TYPE:** Peptide**(iii) HYPOTHETICAL:** No**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** Internal fragment**(vi) ORIGINAL SOURCE:****(A) ORGANISM:** VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB4.

U

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:**

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu  
 1 5 10 15  
 His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile  
 20 25 30  
 Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Gly Ala Arg Gln  
 35 40 45  
 Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr Thr Thr Ala Gly Gly  
 50 55 60  
 Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala  
 65 70 75 80  
 Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg  
 85 90 95  
 Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile Thr Met  
 100 105 110  
 Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Gly Ala Ser Ile  
 115 120 125  
 Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
 130 135 140

**(2) INFORMATION FOR SEQ. ID NO: 19:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH:** 162 Amino acid residues**(B) TYPE:** Amino acid**(C) STRANDEDNESS:** Unknown**(D) TOPOLOGY:** Unknown**(ii) MOLECULE TYPE:** Peptide**(iii) HYPOTHETICAL:** No**(iv) ANTI-SENSE:** No**(v) FRAGMENT TYPE:** Internal fragment**(vi) ORIGINAL SOURCE:****(A) ORGANISM:** VIH-1**(ix) FEATURE:****(D) OTHER INFORMATION:** Multiepitopic polypeptide (MEP) TAB9.**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:**

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
 1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
 20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser  
 35 40 45  
 Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly  
 50 55 60  
 Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr  
 65 70 75 80  
 Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly  
 85 90 95  
 Arg Val Ile Tyr Ala Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His  
 100 105 110  
 Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg  
 115 120 125  
 Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly  
 130 135 140  
 Gly Gly Ala Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val  
 145 150 155 160  
 Thr Ile

(2) INFORMATION FOR SEQ. ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1                      5                      10                      15  
 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
                     20                      25                      30  
 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser  
                     35                      40                      45  
 Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly  
                     50                      55                      60  
  
 Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr  
                     65                      70                      75                      80  
 Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly  
                     85                      90                      95  
 Arg Val Ile Tyr Ala Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His  
                     100                      105                      110  
 Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg  
                     115                      120                      125  
 Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly  
                     130                      135                      140  
 Gly Gly Ala Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Ala Leu Tyr  
                     145                      150                      155                      160  
 Thr Thr Ala Gly Gly Gly Ala Thr Ser Ile Thr Ile Gly Pro Gly Gln  
                     165                      170                      175  
 Val Phe Tyr Arg Thr Gly Ala Gly Gly Gly Ala Ser Ile Arg Ile Gln  
                     180                      185                      190  
 Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
                     195                      200

(2) INFORMATION FOR SEQ. ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

OTHER INFORMATION: Codifies for epitopes V3 linked by the spacer of SEQ ID  
NO: 17: in the  
MEP TAB 19,  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTAGACTCG AGAGGCATTC GTATCGGCCC AGGTCGCGCA  
ATTTTAGCAA CAGCTGGCGG 60

TGGCGCACGT CAATCTACCC CTATTGGTTT AGGTCAGGCT  
CTGTATACGA CTGCCGGCGG 120

TGGTGCGCGC AAAAGTATCA CCAAGGGTCC AGGCCGCGTC  
ATTACGCCA CCGCGGGCGG 180

CGGTGCCCGT AAGCGTATCC ACATTGGCCC AGGCCGTGCA  
TTCTATACTA CAGCAGGTGG 240

TGGCGCACGT AAACGCATCA CTATGGGTCC TGGTCGCGTC  
TATTACACGA CCGCTGGCGG 300

CGGTGCTAGC ATTCGCATCC AACGCGGCCC TGGTCGTGCA  
TTTGTGACCA TATGATAACG 360

CGGGATCC

368